CLAIMS

1. A modified polypeptide containing at least an immunodominant region and the connecting loop between N- and C-helices of gp41 ectodomain of HIV-1, wherein the connecting loop includes at least a linker fragment having:

- a size convenient for keeping the native conformation of the interaction between N- and C-helices, and
- an hydrophily sufficient to provide a soluble and stable trimeric form to said modified polypeptide.

2. The modified polypeptide according to claim 1, wherein said linker is included in substitution of all or only a part of a deleted wildtype oligopeptide along the connecting loop.

3. The modified polypeptide according to claim 1 or 2, wherein said linker is in substitution of a deleted wildtype sequence located in region 598-622, and in particular in region 603 to 615 of SEQ ID NO 1.

4. The modified polypeptide according to claim 1 or 2, wherein said linker is in substitution of a deleted wildtype sequence located in region 525-549, and in particular in region 530 to 542 of SEQ ID NO 14.

5. The modified polypeptide according to anyone of claim 2 to 4, wherein said deleted wildtype oligopeptide has at least 10, in particular 13, and more particularly 25 amino acid residues.

6. The modified polypeptide according to anyone of claims 1 to 5 wherein said linker is an oligopeptide linker.

7. The modified polypeptide according to claim 6, wherein said oligopeptide linker is mainly based on hydrophilic amino acid residues.

8. The modified polypeptide according to any one of the previous claims including as linker fragment, the oligopeptide of SEQ ID NO 2.

9. The modified polypeptide according to anyone of the previous claims including furthermore in its immunodominant region at least one mutation to prevent a cross reaction of the B type and/or of the T type with a host protein.

10. The modified polypeptide according to any one of the previous claims wherein the mutation prevents cross reaction with IL-2.

11. The modified polypeptide according to claim 9 or 10, wherein said mutation is located at least in part of the SEQ ID NO 3, SEQ ID NO 4, SEQ ID NO 5, and/or SEQ ID NO 6.

12. The modified polypeptide according to any one of the previous claims, wherein it may comprises additional modification selected from amino acid residue mutation, deletion and/or insertion for improving solubility of said modified polypeptide.

13. The modified polypeptide according to any one of the previous claims, wherein it is selected from polypeptides of SEQ ID NO 8, SEQ ID NO 17, SEQ ID NO 18, SEQ ID NO 19, and SEQ ID NO 20.

14. The modified polypeptide according to the previous claims, wherein it is the polypeptide of SEQ ID NO 8.

15. The modified polypeptide according to any one of the previous claims, being furthermore an N-truncated oligopeptide, with a length of deletion being of a size ranging from 8 to 15 amino acid residue.

16. The modified polypeptide according to the previous claim, wherein it is truncated in particular of at least 10 amino acid residues, and more particularly of at least 12 amino acid residues at the N-terminal position.

17. The modified polypeptide according to the claims 15 or 16, wherein it is a polypeptide as set forth in SEQ ID NO 21.

18. A polynucleotide encoding the modified polypeptide according to anyone of the claims 1 to 17.

19. The polynucleotide of claim 18 which is DNA.

20. The polynucleotide according to claim 18 or 19, wherein it is a polynucleotide of SEQ ID NO 7.

21. An expression vector comprising at least a transcription promoter, a DNA segment encoding the modified polypeptide according to anyone of claims 1 to 17 and a transcription terminator.

22. A vaccine composition containing at least as active ingredient a modified polypeptide as defined in anyone of claims 1 to 17.